

SEQUENCE LISTING

<110> Reed, John C.
Pio, Frederick F.
Godzik, Adam
Stehlik, Christian
Damiano, Jason S.
Lee, Sug-Hyung
Oliveira, Vasco A.
Hayashi, Hideki
Pawlowski, Krzysztof

<120> Novel Card Domain Containing
Polypeptides, Encoding Nucleic Acids, and Methods of Use

<130> P-LJ 4752

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<151> 2000-05-24

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Lys Leu Leu Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr
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tta act tct cgg agg ctg att tct gag gaa gag tat gag act ctg gag 144
Leu Thr Ser Arg Arg Leu Ile Ser Glu Glu Tyr Glu Thr Leu Glu
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aat gtt aca gat ctc ctg aag aaa agt cgg aag ctg tta att ttg gta 192
Asn Val Thr Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val

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cag aaa aag gga gag gcg acc tgt cag cat ttt ctc aag tgt tta ttt 240
Gln Lys Lys Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys Leu Phe
65 70 75 80

agt act ttt cca cag tca gct gcc att tgc ggc tta agg cat gaa gtt 288
Ser Thr Phe Pro Gln Ser Ala Ala Ile Cys Gly Leu Arg His Glu Val
85 90 95

tta aaa cat gag aat aca gta cct cct caa tct atg ggg gca agc agt 336
Leu Lys His Glu Asn Thr Val Pro Pro Gln Ser Met Gly Ala Ser Ser
100 105 110

aat tca gaa gat gct ttt tct cct gga ata aaa cag cct gaa gcc cct 384
Asn Ser Glu Asp Ala Phe Ser Pro Gly Ile Lys Gln Pro Glu Ala Pro
115 120 125

gag atc aca gtg ttc ttc agt gag aag gaa cac ttg gat ttg gaa acc 432
Glu Ile Thr Val Phe Phe Ser Glu Lys Glu His Leu Asp Leu Glu Thr
130 135 140

tct gag ttt ttc agg gac aag aaa act agt tat agg gaa aca gct ttg 480
Ser Glu Phe Phe Arg Asp Lys Lys Thr Ser Tyr Arg Glu Thr Ala Leu
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Ser Ala Arg Lys Asn Glu Lys Glu Tyr Asp Thr Pro Glu Val Thr Leu
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tca tat tca gtt gag aaa gtt gga tgt gaa gtt cca gca act att aca 576
Ser Tyr Ser Val Glu Lys Val Gly Cys Glu Val Pro Ala Thr Ile Thr
180 185 190

tat ata aaa gat gga cag aga tat gag gag cta gat gat tct tta tac 624
Tyr Ile Lys Asp Gly Gln Arg Tyr Glu Glu Leu Asp Asp Ser Leu Tyr
195 200 205

tta gga aaa gag gaa tat cta gga tct gtt gac acc cct gaa gat gca 672
Leu Gly Lys Glu Glu Tyr Leu Gly Ser Val Asp Thr Pro Glu Asp Ala
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gaa gcc act gtg gaa gag gag gtt tat gat gac cca gag cac gtt gga 720
Glu Ala Thr Val Glu Glu Val Tyr Asp Asp Pro Glu His Val Gly
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tat gat ggt gaa gag gac ttc gag aat tca gaa acc aca gag ttc tct 768
Tyr Asp Gly Glu Glu Asp Phe Glu Asn Ser Glu Thr Thr Glu Phe Ser
245 250 255

ggt gaa gaa cca agt tat gag gga tca gaa acc agc ctt tca ttg gag 816
Gly Glu Glu Pro Ser Tyr Glu Gly Ser Glu Thr Ser Leu Ser Leu Glu
260 265 270

gag gaa cag gag aaa agt ata gaa ggc tgg tct cga act cat ggg ctt 864
Glu Glu Gln Glu Lys Ser Ile Glu Gly Trp Ser Arg Thr His Gly Leu
275 280 285

aag cga tcc tcc cac gtt ggc ctc cca aag tgc tgg gat tac agg cgt 912
Lys Arg Ser Ser His Val Gly Leu Pro Lys Cys Trp Asp Tyr Arg Arg
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35 40 45
Asn Val Thr Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val
50 55 60
Gln Lys Lys Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys Leu Phe
65 70 75 80
Ser Thr Phe Pro Gln Ser Ala Ala Ile Cys Gly Leu Arg His Glu Val
85 90 95
Leu Lys His Glu Asn Thr Val Pro Pro Gln Ser Met Gly Ala Ser Ser
100 105 110
Asn Ser Glu Asp Ala Phe Ser Pro Gly Ile Lys Gln Pro Glu Ala Pro
115 120 125
Glu Ile Thr Val Phe Phe Ser Glu Lys Glu His Leu Asp Leu Glu Thr
130 135 140
Ser Glu Phe Phe Arg Asp Lys Lys Thr Ser Tyr Arg Glu Thr Ala Leu
145 150 155 160
Ser Ala Arg Lys Asn Glu Lys Glu Tyr Asp Thr Pro Glu Val Thr Leu
165 170 175
Ser Tyr Ser Val Glu Lys Val Gly Cys Glu Val Pro Ala Thr Ile Thr
180 185 190
Tyr Ile Lys Asp Gly Gln Arg Tyr Glu Glu Leu Asp Asp Ser Leu Tyr
195 200 205
Leu Gly Lys Glu Glu Tyr Leu Gly Ser Val Asp Thr Pro Glu Asp Ala
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Glu Ala Thr Val Glu Glu Glu Val Tyr Asp Asp Pro Glu His Val Gly
225 230 235 240
Tyr Asp Gly Glu Glu Asp Phe Glu Asn Ser Glu Thr Thr Glu Phe Ser

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Gly Glu Glu Pro Ser Tyr Glu Gly Ser	Glu Thr Ser Leu Ser	Leu Glu
260	265	270
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Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu
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gac tgg ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc 144
Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly
35 40 45

tcc cac ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg 192
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu
50 55 60

gac acc gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc atc gcg 240
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala
65 70 75 80

gct gcc caa gaa gcc cag gcc gac agc cag tcc ccc aag ctg cat ggc 288
Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly
85 90 95

tgc tgg gac ccc cac tcg ctc cac cca gcc cga gac ctg cag agt cac 336
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His
100 105 110

cgg cca gcc att gtc agg agg ctc cac agc cat gtg gag aac atg ctg 384
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu
115 120 125

gac ctg gca tgg gag cgg ggt ttc gtc agc cag tat gaa tgt gat gaa 432
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu
130 135 140

atc agg ttg ccg atc ttc aca ccg tcc cag agg gca aga agg ctg ctt 480
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu
145 150 155 160

gat ctt gcc acg gtg aaa gcg aat gga ttg gct gcc ttc ctt cta caa 528
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln
165 170 175

cat gtt cag gaa tta cca gtc cca ttg gcc ctg cct ttg gaa gct gcc 576
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala
180 185 190

aca tgc aag aag tat atg gcc aag ctg agg acc acg gtg tct gct cag 624
Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Val Ser Ala Gln
195 200 205

tct cgc ttc ctc agt acc tat tat gat gga gca gag acg ctc tgc ctg gag 672
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu
210 215 220

gac ata tac aca gag aat gtc ctg gag gtc tgg gca gat gtg ggc atg 720
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met
225 230 235 240

gct gga ccc ccg cag aag agc cca gcc acc ctg ggc ctg gag gag ctc 768
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu
245 250 255

ttc agc acc cct ggc cac ctc aat gac gat gcg gac act gtg ctg gtg 816
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val
260 265 270

gtg ggt gag ggc agt ggc aag agc acg ctc ctg cag cgg ctg cac 864

Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His
275 280 285

ttg ctg tgg gct gca ggg caa gac ttc cag gaa ttt ctc ttt gtc ttc 912
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe
290 295 300

cca ttc agc tgc cgg cag ctg cag tgc atg gcc aaa cca ctc tct gtg 960
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val
305 310 315 320

cgg act cta ctc ttt gag cac tgc tgt tgg cct gat gtt ggt caa gaa 1008
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu
325 330 335

gac atc ttc cag tta ctc ctt gac cac cct gac cgt gtc ctg tta acc 1056
Asp Ile Phe Gln Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr
340 345 350

ttt gat ggc ttt gac gag ttc aag ttc agg ttc acg gat cgt gaa cgc 1104
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg
355 360 365

cac tgc tcc ccg acc gac ccc acc tct gtc cag acc ctg ctc ttc aac 1152
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn
370 375 380

ctt ctg cag ggc aac ctg ctg aag aat gcc cgc aag gtg gtg acc agc 1200
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser
385 390 395 400

cgt ccg gcc gct gtg tcg gcg ttc ctc agg aag tac atc cgc acc gag 1248
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu
405 410 415

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Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg
420 425 430

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Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu
435 440 445

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Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser
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tgg atg gtg tcc aaa tgc cac cag gaa ctg ttg ctg cag gag ggg ggg 1440
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Gln Glu Gly Gly
465 470 475 480

tcc cca aag acc act aca gat atg tac ctg ctg att ctg cag cat ttt 1488
Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe

485

490

495

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Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln
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<212> PRT

<213> Homo sapien

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Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly

DRAFT - 05/2002

35 40 45
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu
50 55 60
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala
65 70 75 80
Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly
85 90 95
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His
100 105 110
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu
115 120 125
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu
130 135 140
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu
145 150 155 160
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln
165 170 175
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala
180 185 190
Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln
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Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu
210 215 220
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met
225 230 235 240
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu
245 250 255
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val
260 265 270
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His
275 280 285
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe
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Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val
305 310 315 320
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu
325 330 335
Asp Ile Phe Gln Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr
340 345 350
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg
355 360 365
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn
370 375 380
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser
385 390 395 400
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu
405 410 415
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg
420 425 430
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu
435 440 445
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser
450 455 460

Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Leu Gln Glu Gly Gly
465 470 475 480
Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe
485 490 495
Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro
500 505 510
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu
515 520 525
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530 535 540
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu
545 550 555 560

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gagaaggaac acttgattt ggaaacacctt gagttttca gggacaagaa aactagttat 540
agggaaacag ctgttgc tgc caggaagaat gagaaggaat atgacacacc agaagtcaca 600
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ctccccaaagt gctggatgtt caggcgttag ccaccctgcc tggcctgaaa attctgcctc 1020
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Phe Ile His Ser Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu
15 20 25

tta tta cag aca agg gtg ctg aac cag gaa gag atg gag aaa gta aaa 146
Leu Leu Gln Thr Arg Val Leu Asn Gln Glu Glu Met Lys Val Lys
30 35 40

cgt gaa aat gct aca gtt atg gat aag acc cga gct ttg att gac tcc 194
Arg Glu Asn Ala Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser
45 50 55 60

gtt att ccg aaa ggg gca cag gca tgc caa att tgc atc aca tac att 242
Val Ile Pro Lys Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile
65 70 75

tgt gaa gaa gac agt tac ctg gca gag acg ctg gga ctc tca gca ggt 290
Cys Glu Glu Asp Ser Tyr Leu Ala Glu Thr Leu Gly Leu Ser Ala Gly
80 85 90

ccg ata cct gga aat tagcttagct tagtacacaa gactcccaat tactatttc 345
Pro Ile Pro Gly Asn
95

tcccttcca gctttcagg cagtgcagga caaccagct atgcccacat gctcaagccc 405
agaaggcaga atcaagctt gctttctaga agacgctcaa aggatatgga aacaaaagtt 465
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<211> 97

<212> PRT

<213> Homo sapien

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Arg Val Leu Asn Gln Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala
35 40 45

Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys
50 55 60

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Ser Tyr Leu Ala Glu Thr Leu Gly Leu Ser Ala Gly Pro Ile Pro Gly
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Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala
   35          40          45
Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys
   50          55          60
Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp
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85 90 95

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100 105

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Ser Gln Glu Asp Thr Glu Ile Val Lys Cys Glu Asn Val Thr Val Ile
35 40 45
Asp Lys Ala Arg Asp Leu Leu Asp Ser Val Ile Arg Lys Gly Ala Gly
50 55 60
Ala Cys Glu Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp Arg Tyr Leu
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85 90 95
Ile Cys Ser Pro Pro Arg Ala Gln Asp Leu
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Asn Val Leu Ser Gln Glu Asp Glu Ile Val Lys Arg Glu Asn Ala Thr
35 40 45
Val Ile Asp Lys Ala Arg Ala Leu Leu Asp Ser Val Ile Arg Lys Gly
50 55 60
Ala Gly Ala Cys Glu Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp Ser
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DRAFT GENOME

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aaaagaggac aatattggga tcaccttga cctttccatt tggaaataat attttctatt 240
gtgttataga aaggtggaa gcttcatcc agaaca atg aat ttc ata aag gac 294
Met Asn Phe Ile Lys Asp
1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
40 45 50

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Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu
55 60 65 70

aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly
75 80 85

caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct 582
Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala
90 95 100

cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat 630
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr
105 110 115

ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc 678
Pro Leu Gly Glu Asp Ile Asp Ile Phe Asn Leu Lys Ser Thr Phe
120 125 130

aca gaa cct atc ctg tgg agg aag gac caa cac cat cac cgc gtg gag 726
Thr Glu Pro Ile Leu Trp Arg Lys Asp Gln His His Arg Val Glu
135 140 145 150

cag ctg acc ctg aat ggc ctc ctg cag gct ctt cag agc ccc tgc atc 774
Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser Pro Cys Ile
155 160 165

att gaa ggg gaa tct ggc aaa ggc aag tcc act ctg ctg cag cgc att 822
Ile Glu Gly Glu Ser Gly Lys Ser Thr Leu Leu Gln Arg Ile
170 175 180

gcc atg ctc tgg ggc tcc gga aag tgc aag gct ctg acc aag ttc aaa 870
Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr Lys Phe Lys
185 190 195

ttc gtc ttc ttc ctc cgt ctc agc agg gcc cag ggt gga ctt ttt gaa 918
Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Leu Phe Glu
200 205 210

acc ctc tgt gat caa ctc ctg gat ata cct ggc aca atc agg aag cag 966
Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro Gly Thr Ile Arg Lys Gln
215 220 225 230

aca ttc atg gcc atg ctg ctg aag ctg cgg cag agg gtt ctt ttc ctt 1014
Thr Phe Met Ala Met Leu Leu Lys Leu Arg Gln Arg Val Leu Phe Leu
235 240 245

ctt gat ggc tac aat gaa ttc aag ccc cag aac tgc cca gaa atc gaa 1062
Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln Asn Cys Pro Glu Ile Glu
250 255 260

gcc ctg ata aag gaa aac cac cgc ttc aag aac atg gtc atc gtc acc 1110
Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val Ile Val Thr

265 270 275
act acc act gag tgc ctg agg cac ata cgg cag ttt ggt gcc ctg act 1158
Thr Thr Thr Glu Cys Leu Arg His Ile Arg Gln Phe Gly Ala Leu Thr
280 285 290

gct gag gtg ggg gat atg aca gaa gac agc gcc cag gct ctc atc cga 1206
Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala Leu Ile Arg
295 300 305 310

gaa gtg ctg atc aag gag ctt gct gaa ggc ttg ttg ctc caa att cag 1254
Glu Val Leu Ile Lys Glu Leu Ala Glu Gly Leu Leu Leu Gln Ile Gln
315 320 325

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Lys Ser Arg Cys Leu Arg Asn Leu Met Lys Thr Pro Leu Phe Val Val
330 335 340

atc act tgt gca atc cag atg ggt gaa agt gag ttc cac tct cac aca 1350
Ile Thr Cys Ala Ile Gln Met Gly Glu Ser Glu Phe His Ser His Thr
345 350 355

caa aca acg ctg ttc cat acc ttc tat gat ctg ttg ata cag aaa aac 1398
Gln Thr Thr Leu Phe His Thr Phe Tyr Asp Leu Leu Ile Gln Lys Asn
360 365 370

aaa cac aaa cat aaa ggt gtg gct gca agt gac ttc att cgg agc ctg 1446
Lys His Lys His Lys Gly Val Ala Ala Ser Asp Phe Ile Arg Ser Leu
375 380 385 390

gac cac cgt gga gac cta gct ctg gag ggt gtg ttc tcc cac aag ttt 1494
Asp His Arg Gly Asp Leu Ala Leu Glu Gly Val Phe Ser His Lys Phe
395 400 405

gat ttc gaa ctg cag gat gtg tcc agc gtg aat gag gat gtc ctg ctg 1542
Asp Phe Glu Leu Gln Asp Val Ser Ser Val Asn Glu Asp Val Leu Leu
410 415 420

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Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala Gln Arg Phe Lys Pro Lys
425 430 435

tat aaa ttc ttt cac aag tca ttc cag gag tac aca gca gga cga aga 1638
Tyr Lys Phe Phe His Lys Ser Phe Gln Glu Tyr Thr Ala Gly Arg Arg
440 445 450

ctc agc agt tta ttg acg tct cat gag cca gag gag gtg acc aag ggg 1686
Leu Ser Ser Leu Leu Thr Ser His Glu Pro Glu Glu Val Thr Lys Gly
455 460 465 470

aat ggt tac ttg cag aaa atg gtt tcc att tcg gac att aca tcc act 1734
Asn Gly Tyr Leu Gln Lys Met Val Ser Ile Ser Asp Ile Thr Ser Thr
475 480 485

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caa agt gtg aaa aac acc act gag caa gaa att ctg aaa gcc ata aac Gln Ser Val Lys Asn Thr Thr Glu Gln Glu Ile Leu Lys Ala Ile Asn 535 540 545 550	1926
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ttt gaa cat ttg ccc aat t ^g t gca agt gcc ctg gac ttc att aaa ctg Phe Glu His Leu Pro Asn Cys Ala Ser Ala Leu Asp Phe Ile Lys Leu 600 605 610	2118
gac ttt tat ggg gga gct atg gct tca tgg gaa aag gct gca gaa gac Asp Phe Tyr Gly Gly Ala Met Ala Ser Trp Glu Lys Ala Ala Glu Asp 615 620 625 630	2166
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Cys Lys Asn Ile Tyr Ser Leu Met Val Glu Ala Ser Pro Leu Thr Ile
715 720 725
gaa gat gag agg cac atc aca tct gta aca aac ctg aaa acc ttg agt 2502
Glu Asp Glu Arg His Ile Thr Ser Val Thr Asn Leu Lys Thr Leu Ser
730 735 740
att cat gac cta cag aat caa cgg ctg ccg ggt ggt ctg act gac agc 2550
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745 750 755
ttg ggt aac ttg aag aac ctt aca aag ctc ata atg gat aac ata aag 2598
Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys
760 765 770
atg aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg 2646
Met Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu
775 780 785 790
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Lys Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu
795 800 805
gga atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt 2742
Gly Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu
810 815 820
gaa gaa att caa tta gtc tcc tgc tgc ttg tct gca aat gca gtg aaa 2790
Glu Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys
825 830 835
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840 845 850
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855 860 865 870
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875 880 885
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Pro Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His
890 895 900
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905 910 915

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920 925 930

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Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser
935 940 945 950

agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag caa 3174
Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln
955 960 965

tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct gat cca gca 3222
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970 975 980

tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act ttt ctg caa 3270
Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln
985 990 995

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Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
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Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
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Phe Gln Asp Leu Asn Gly Gln Ser Leu Phe His Gln Thr Ser Glu Gly
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Asp Leu Asp Asp Leu Ala Gln Asp Leu Lys Asp Leu Tyr His Thr Pro
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Ser Phe Leu Asn Phe Tyr Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe
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Asn Leu Lys Ser Thr Phe Thr Glu Pro Ile Leu Trp Arg Lys Asp Gln
130 135 140
His His His Arg Val Glu Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala
145 150 155 160
Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser
165 170 175
Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys
180 185 190
Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala
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Gln Gly Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro
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Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg
225 230 235 240
Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln
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260 265 270
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275 280 285
Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser
290 295 300
Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly
305 310 315 320
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325 330 335
Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser
340 345 350
Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp
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Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser
370 375 380
Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly
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Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val
405 410 415
Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala
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Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu
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Tyr Thr Ala Gly Arg Arg Leu Ser Ser Leu Leu Thr Ser His Glu Pro
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Glu Glu Val Thr Lys Gly Asn Gly Tyr Leu Gln Lys Met Val Ser Ile
465 470 475 480
Ser Asp Ile Thr Ser Thr Tyr Ser Ser Leu Leu Arg Tyr Thr Cys Gly
485 490 495
Ser Ser Val Glu Ala Thr Arg Ala Val Met Lys His Leu Ala Ala Val
500 505 510
Tyr Gln His Gly Cys Leu Leu Gly Leu Ser Ile Ala Lys Arg Pro Leu
515 520 525
Trp Arg Gln Glu Ser Leu Gln Ser Val Lys Asn Thr Thr Glu Gln Glu

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565 570 575
Ala Phe Phe Gln Gly Lys Ser Leu Tyr Ile Asn Ser Gly Asn Ile Pro
580 585 590
Asp Tyr Leu Phe Asp Phe Glu His Leu Pro Asn Cys Ala Ser Ala
595 600 605
Leu Asp Phe Ile Lys Leu Asp Phe Tyr Gly Gly Ala Met Ala Ser Trp
610 615 620
Glu Lys Ala Ala Glu Asp Thr Gly Gly Ile His Met Glu Glu Ala Pro
625 630 635 640
Glu Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys
645 650 655
Gln Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu
660 665 670
Asn Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr
675 680 685
Ser Leu Arg Leu Gln Ile Lys Arg Cys Ala Gly Val Ala Gly Ser Leu
690 695 700
Ser Leu Val Leu Ser Thr Cys Lys Asn Ile Tyr Ser Leu Met Val Glu
705 710 715 720
Ala Ser Pro Leu Thr Ile Glu Asp Glu Arg His Ile Thr Ser Val Thr
725 730 735
Asn Leu Lys Thr Leu Ser Ile His Asp Leu Gln Asn Gln Arg Leu Pro
740 745 750
Gly Gly Leu Thr Asp Ser Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu
755 760 765
Ile Met Asp Asn Ile Lys Met Asn Glu Glu Asp Ala Ile Lys Leu Ala
770 775 780
Glu Gly Leu Lys Asn Leu Lys Lys Met Cys Leu Phe His Leu Thr His
785 790 795 800
Leu Ser Asp Ile Gly Glu Gly Met Asp Tyr Ile Val Lys Ser Leu Ser
805 810 815
Ser Glu Pro Cys Asp Leu Glu Glu Ile Gln Leu Val Ser Cys Cys Leu
820 825 830
Ser Ala Asn Ala Val Lys Ile Leu Ala Gln Asn Leu His Asn Leu Val
835 840 845
Lys Leu Ser Ile Leu Asp Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly
850 855 860
Asn Glu Ala Leu His Glu Leu Ile Asp Arg Met Asn Val Leu Glu Gln
865 870 875 880
Leu Thr Ala Leu Met Leu Pro Trp Gly Cys Asp Val Gln Gly Ser Leu
885 890 895
Ser Ser Leu Leu Lys His Leu Glu Glu Val Pro Gln Leu Val Lys Leu
900 905 910
Gly Leu Lys Asn Trp Arg Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly
915 920 925
Ala Phe Phe Gly Lys Asn Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu
930 935 940
Ala Gly Asn Arg Val Ser Ser Asp Gly Trp Leu Ala Phe Met Gly Val
945 950 955 960

Phe Glu Asn Leu Lys Gln Leu Val Phe Phe Asp Phe Ser Thr Lys Glu
965 970 975
Phe Leu Pro Asp Pro Ala Leu Val Arg Lys Leu Ser Gln Val Leu Ser
980 985 990
Lys Leu Thr Phe Leu Gln Glu Ala Arg Leu Val Gly Trp Gln Phe Asp
995 1000 1005
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acatctgctg gaagtcctct gggattcaag gtacaggaa tgaagagtag tttacagaa 180
aaaagaggac aatattggga tcaccttga ccttccatt tggaaataat atttctatt 240
gtgttataga aaggtggaa gcttcatcc agaaca atg aat ttc ata aag gac 294
Met Asn Phe Ile Lys Asp
1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
40 45 50

att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 486
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu
55 60 65 70

aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly
75 80 85

caa agt ggt ctg act gac agc ttg ggt aac ttg aag aac ctt aca aag 582
Gln Ser Gly Leu Thr Asp Ser Leu Gly Asn Leu Lys Asn Leu Thr Lys
90 95 100

ctc ata atg gat aac ata aag atg aat gaa gaa gat gct ata aaa cta 630

Leu Ile Met Asp Asn Ile Lys Met Asn Glu Glu Asp Ala Ile Lys Leu
105 110 115

gct gaa ggc ctg aaa aac ctg aag aag atg tgt tta ttt cat ttg acc 678
Ala Glu Gly Leu Lys Asn Leu Lys Lys Met Cys Leu Phe His Leu Thr
120 125 130

cac ttg tct gac att gga gag gga atg gat tac ata gtc aag tct ctg 726
His Leu Ser Asp Ile Gly Glu Gly Met Asp Tyr Ile Val Lys Ser Leu
135 140 145 150

tca agt gaa ccc tgt gac ctt gaa gaa att caa tta gtc tcc tgc tgc 774
Ser Ser Glu Pro Cys Asp Leu Glu Glu Ile Gln Leu Val Ser Cys Cys
155 160 165

ttg tct gca aat gca gtg aaa atc cta gct cag aat ctt cac aat ttg 822
Leu Ser Ala Asn Ala Val Lys Ile Leu Ala Gln Asn Leu His Asn Leu
170 175 180

gtc aaa ctg agc att ctt gat tta tca gaa aat tac ctg gaa aaa gat 870
Val Lys Leu Ser Ile Leu Asp Leu Ser Glu Asn Tyr Leu Glu Lys Asp
185 190 195

gga aat gaa gct ctt cat gaa ctg atc gac agg atg aac gtg cta gaa 918
Gly Asn Glu Ala Leu His Glu Leu Ile Asp Arg Met Asn Val Leu Glu
200 205 210

cag ctc acc gca ctg atg ctg ccc tgg ggc tgt gac gtg caa ggc agc 966
Gln Leu Thr Ala Leu Met Leu Pro Trp Gly Cys Asp Val Gln Gly Ser
215 220 225 230

ctg agc agc ctg ttg aaa cat ttg gag gag gtc cca caa ctc gtc aag 1014
Leu Ser Ser Leu Leu Lys His Leu Glu Glu Val Pro Gln Leu Val Lys
235 240 245

ctt ggg ttg aaa aac tgg aga ctc aca gat aca gag att aga att tta 1062
Leu Gly Leu Lys Asn Trp Arg Leu Thr Asp Thr Glu Ile Arg Ile Leu
250 255 260

ggg gca ttt ttt gga aag aac cct ctg aaa aac ttc cag cag ttg aat 1110
Gly Ala Phe Phe Gly Lys Asn Pro Leu Lys Asn Phe Gln Gln Leu Asn
265 270 275

ttg gcg gga aat cgt gtg agc agt gat gga tgg ctt gcc ttc atg ggt 1158
Leu Ala Gly Asn Arg Val Ser Ser Asp Gly Trp Leu Ala Phe Met Gly
280 285 290

gta ttt gag aat ctt aag caa tta gtg ttt ttt gac ttt agt act aaa 1206
Val Phe Glu Asn Leu Lys Gln Leu Val Phe Phe Asp Phe Ser Thr Lys
295 300 305 310

gaa ttt cta cct gat cca gca tta gtc aga aaa ctt agc caa gtg tta 1254
Glu Phe Leu Pro Asp Pro Ala Leu Val Arg Lys Leu Ser Gln Val Leu

315

320

325

tcc aag tta act ttt ctg caa gaa gct agg ctt gtt ggg tgg caa ttt 1302
Ser Lys Leu Thr Phe Leu Gln Glu Ala Arg Leu Val Gly Trp Gln Phe
330 335 340

gat gat gat gat ctc agt gtt att aca ggt gct ttt aaa cta gta act 1350
Asp Asp Asp Asp Leu Ser Val Ile Thr Gly Ala Phe Lys Leu Val Thr
345 350 355

gct taaataaaagt gtactcgaag caaaaaaaaaaaa aaaaaaaaaaa aa 1395
Ala

<210> 99
<211> 359
<212> PRT
<213> Homo sapien

Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
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Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val
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Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80
Phe Gln Asp Leu Asn Gly Gln Ser Gly Leu Thr Asp Ser Leu Gly Asn
85 90 95
Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met Asn Glu
100 105 110
Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys Lys Met
115 120 125
Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly Met Asp
130 135 140
Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu Glu Ile
145 150 155 160
Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile Leu Ala
165 170 175
Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu Ser Glu
180 185 190
Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu Ile Asp
195 200 205
Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro Trp Gly
210 215 220
Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu Glu Glu
225 230 235 240
Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu Thr Asp
245 250 255

Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro Leu Lys
260 265 270
Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser Asp Gly
275 280 285
Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln Leu Val Phe
290 295 300
Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala Leu Val Arg
305 310 315 320
Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln Glu Ala Arg
325 330 335
Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val Ile Thr Gly
340 345 350
Ala Phe Lys Leu Val Thr Ala
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<211> 578

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (277) ... (552)

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acatctgctg gaagtccctc gggattcaag gtacaggaa tgaagagtag ttacagaa 180
aaaagaggac aatattggga tcaccttga ccttccatt tggaaataat attttctatt 240
gtgttataga aaggtggaa gcttcatcc agaaca atg aat ttc ata aag gac 294
Met Asn Phe Ile Lys Asp
1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
40 45 50

att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 486
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu
55 60 65 70

aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly
75 80 85

caa agt ctt tta aca gct tagaaagtac agtagacata ctgggg 578
Gln Ser Leu Leu Thr Ala
90

<210> 101
<211> 92
<212> PRT
<213> Homo sapien

<400> 101
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
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Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val
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Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80
Phe Gln Asp Leu Asn Gly Gln Ser Leu Leu Thr Ala
85 90

<210> 102
<211> 768
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (277) ... (744)

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acatctgctg gaagtccctct gggattcaag gtacaggaa tgaagagtag tttacagaa 180
aaaagaggac aatattggaa tcaccttga ccttccatt tggaaataat atttctatt 240
gtgttataga aaggtggaa gctttcatcc agaaca atg aat ttc ata aag gac 294
Met Asn Phe Ile Lys Asp
1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438

Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
40 45 50

att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 486
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu
55 60 65 70

aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly
75 80 85

caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct 582
Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala
90 95 100

cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat 630
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr
105 110 115

ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc 678
Pro Leu Gly Glu Asp Ile Asp Ile Phe Asn Leu Lys Ser Thr Phe
120 125 130

aca gaa cct gtc ctg tgg agg aag gac caa cac cat cac cgc gtg gag 726
Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His Arg Val Glu
135 140 145 150

cag ctg acc cta gtt tta tagcatcttc tacctgccccg ggcg 768
Gln Leu Thr Leu Val Leu
155

<210> 103
<211> 156
<212> PRT
<213> Homo sapien

<400> 103
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
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Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val
20 25 30
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80
Phe Gln Asp Leu Asn Gly Gln Ser Leu Phe His Gln Thr Ser Glu Gly
85 90 95
Asp Leu Asp Asp Leu Ala Gln Asp Leu Lys Asp Leu Tyr His Thr Pro
100 105 110
Ser Phe Leu Asn Phe Tyr Pro Leu Gly Glu Asp Ile Asp Ile Phe

115 120 125
Asn Leu Lys Ser Thr Phe Thr Glu Pro Val Leu Trp Arg Lys Asp Gln
130 135 140
His His His Arg Val Glu Gln Leu Thr Leu Val Leu
145 150 155

<210> 104
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 104
aagaagagac ggctgcttat caat

24

<210> 105
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 105
ccacagcagg cctcgaagat gatc

24

<210> 106
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 106
atgatcctcc tgaagaagag

20

<210> 107
<211> 1009
<212> PRT
<213> Homo sapien

<400> 107
Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu
1 5 10 15
Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu
20 25 30
Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly
35 40 45
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu

50 55 60
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala
65 70 75 80
Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly
 85 90 95
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His
 100 105 110
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu
 115 120 125
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu
 130 135 140
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu
145 150 155 160
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln
 165 170 175
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala
 180 185 190
Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln
 195 200 205
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu
 210 215 220
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met
225 230 235 240
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu
 245 250 255
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val
 260 265 270
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His
 275 280 285
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe
 290 295 300
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val
305 310 315 320
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu
 325 330 335
Asp Ile Phe Gln Leu Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr
 340 345 350
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg
 355 360 365
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn
 370 375 380
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser
 385 390 395 400
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu
 405 410 415
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg
 420 425 430
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu
 435 440 445
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser
 450 455 460
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Gln Glu Gly Gly
465 470 475 480

Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe
485 490 495
Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro
500 505 510
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu
515 520 525
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln
530 535 540
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu
545 550 555 560
Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe
565 570 575
Leu His Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu
580 585 590
Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly
595 600 605
Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile
610 615 620
Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys
625 630 635 640
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu
645 650 655
Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu
660 665 670
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg
675 680 685
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu
690 695 700
Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser
705 710 715 720
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly
725 730 735
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr
740 745 750
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val
755 760 765
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln
770 775 780
Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu Tyr Leu Arg Asp Asn
785 790 795 800
Asn Ile Ser Asp Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His
805 810 815
Cys Glu Gln Leu Gln Lys Leu Ala Leu Gly Asn Asn Tyr Ile Thr Ala
820 825 830
Ala Gly Ala Gln Val Leu Ala Glu Gly Leu Arg Gly Asn Thr Ser Leu
835 840 845
Gln Phe Leu Gly Phe Trp Gly Asn Arg Val Gly Asp Glu Gly Ala Gln
850 855 860
Ala Leu Ala Glu Ala Leu Gly Asp His Gln Ser Leu Arg Trp Leu Ser
865 870 875 880
Leu Val Gly Asn Asn Ile Gly Ser Val Gly Ala Gln Ala Leu Ala Leu
885 890 895
Met Leu Ala Lys Asn Val Met Leu Glu Glu Leu Cys Leu Glu Glu Asn

DRAFT - 05/23/02

900	905	910
His Leu Gln Asp Glu Gly Val Cys Ser Leu Ala Glu Gly Leu Lys Lys		
915	920	925
Asn Ser Ser Leu Lys Ile Leu Asn Ile Lys Ile His Ala Ser Gly Phe		
930	935	940
Asn Lys Leu Leu Glu Ser Ile Phe Cys Ile Leu Leu Val Val Glu Ala		
945	950	955
Phe Phe Leu Gln Lys Val Val Lys Ile Leu Glu Glu Met Val Val Ser		
965	970	975
Trp Leu Glu Val Arg Leu Ser Asn Asn Cys Ile Thr Tyr Leu Gly Ala		
980	985	990
Glu Ala Leu Leu Gln Ala Leu Glu Arg Asn Asp Thr Ile Leu Glu Val		
995	1000	1005
Trp		

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<211> 30

<212> DNA

<213> Artificial Sequence

<220>
<223> primer

<400> 145
ccagaattca tggccgacaa ggtcctgaag 30

<210> 146
<211> 30
<212> DNA
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<220>
<223> primer

<400> 146
ccactcgagc taatttccag gtatcggacc 30

<210> 147
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 147
gaagacagtt acctggcaga 20

<210> 148
<211> 21
<212> DNA
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<220>
<223> primer

<400> 148
ttgtattctg aacatggcac c 21

<210> 149
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<400> 149
gatcatcatc caggccgccc gtgggtgacag ccctgg 36

<210> 150
<211> 36
<212> DNA

02264921 * 052311
<213> Artificial Sequence
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<400> 150
ccaggcgtt caccacgggc ggcctggatg atgatc 36

<210> 151
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 151
cggaattcat gcccgacaag gtcctg 26

<210> 152
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 152
cgctcgagtt agtcttgcat attaaggtaa tttccaga 38

<210> 153
<211> 23
<212> DNA
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<220>
<223> primer

<400> 153
catgtaatg atccctctag cag 23

<210> 154
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 154
gggctcggtt atcgtgtct a 21

<210> 155

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 155
acgatagccg agcccttatt c

21

<210> 156
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 156
gtatggaatg ttctgaatcg c

21

<210> 157
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 157
cccggtatcca tgaatttcat aaaggacaat agc

33

<210> 158
<211> 30
<212> DNA
<213> Artificial Sequence

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<223> primer

<400> 158
cccttcgaac aagtccctgaa atagaggata

30

<210> 159
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 159
ggtgaggcag gatgctgcta gagg

24

<210> 160
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 160
cacagtggc caggctccga atgaagtca 29

<210> 161
<211> 25
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<220>
<223> primer

<400> 161
catcatttgc tgcgagaagg tggag 25

<210> 162
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<400> 162
ttaacttgg taacacttgg ctaag 25

<210> 163
<211> 23
<212> DNA
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<220>
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<400> 163
gtaaacatca tttgctgcga gaa 23

<210> 164
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cccgccagg tagaagatgc tat 23

<210> 165
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 165
aatttcataa aggacaatag ccgag 25

<210> 166
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 166
tgtctactgt actttctaag ctgtt 25

<210> 167
<211> 225
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (225)

<400> 167
gag agt act ccc tca gag atc ata gaa aga gaa aga aaa aag ttg ctt 48
Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys Lys Leu Leu
1 5 10 15

gaa atc ctt caa cat gat cct gat tct atc tta gac acg tta act tct 96
Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser
20 25 30

cgg agg ctg att tct gag gaa gag tat gag act ctg gag aat gtt aca 144
Arg Arg Leu Ile Ser Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr
35 40 45

gat ctc ctg aag aaa agt cgg aag ctg tta att ttg gta cag aaa aag 192
Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys
50 55 60

gga gag gcg acc tgt cag cat ttt ctc aag tgt 225
Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys

65

70

75

<210> 168
<211> 75
<212> PRT
<213> Homo sapiens

<400> 168
Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys Lys Leu Leu
1 5 10 15
Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser
20 25 30
Arg Arg Leu Ile Ser Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr
35 40 45
Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys
50 55 60
Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys
65 70 75

<210> 169
<211> 228
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(228)

<400> 169
atg tgc tcg cag gag gct ttt cag gca cag agg agc cag ctg gtc gag 48
Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu
1 5 10 15

ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg gac tgg 96
Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp
20 25 30

ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc ttc cac 144
Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His
35 40 45

ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg gac acc 192
Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr
50 55 60

gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc 228
Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu
65 70 75

<210> 170

<211> 76
<212> PRT
<213> Homo sapiens

<400> 170
Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu
1 5 10 15
Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp
20 25 30
Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His
35 40 45
Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr
50 55 60
Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu
65 70 75

<210> 171
<211> 243
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(243)

<400> 171
cca gcc cga gac ctg cag agt cac cgg cca gcc att gtc agg agg ctc 48
Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg Leu
1 5 10 15

cac agc cat gtg gag aac atg ctg gac ctg gca tgg gag cgg ggt ttc 96
His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly Phe
20 25 30

gtc agc cag tat gaa tgt gat gaa atc agg ttg ccg atc ttc aca ccg 144
Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr Pro
35 40 45

tcc cag agg gca aga agg ctg ctt gat ctt gcc acg gtg aaa gcg aat 192
Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu Ala Thr Val Lys Ala Asn
50 55 60

gga ttg gct gcc ttc ctt cta caa cat gtt cag gaa tta cca gtc cca 240
Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val Pro
65 70 75 80

ttg 243
Leu

<210> 172

<211> 81
<212> PRT
<213> Homo sapiens

<400> 172
Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg Leu
1 5 10 15
His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly Phe
20 25 30
Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr Pro
35 40 45
Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu Ala Thr Val Lys Ala Asn
50 55 60
Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val Pro
65 70 75 80
Leu

DRAFT

<210> 173
<211> 888
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (888)

<400> 173
gac gat gcg gac act gtg ctg gtg ggt gag gcg ggc agt ggc aag 48
Asp Asp Ala Asp Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly Lys
1 5 10 15
agc acg ctc ctg cag cgg ctg cac ttg ctg tgg gct gca ggg caa gac 96
Ser Thr Leu Leu Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln Asp
20 25 30
ttc cag gaa ttt ctc ttt gtc ttc cca ttc agc tgc cgg cag ctg cag 144
Phe Gln Glu Phe Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu Gln
35 40 45
tgc atg gcc aaa cca ctc tct gtg cgg act cta ctc ttt gag cac tgc 192
Cys Met Ala Lys Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His Cys
50 55 60
tgt tgg cct gat gtt ggt caa gaa gac atc ttc cag tta ctc ctt gac 240
Cys Trp Pro Asp Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Asp
65 70 75 80
cac cct gac cgt gtc ctg tta acc ttt gat ggc ttt gac gag ttc aag 288
His Pro Asp Arg Val Leu Leu Thr Phe Asp Gly Phe Asp Glu Phe Lys
85 90 95

ttc agg ttc acg gat cgt gaa cgcc cac tgc tcc ccg acc gac ccc acc 336
Phe Arg Phe Thr Asp Arg Glu Arg His Cys Ser Pro Thr Asp Pro Thr
100 105 110

tct gtc cag acc ctg ctc ttc aac ctt ctg cag ggc aac ctg ctg aag 384
Ser Val Gln Thr Leu Leu Phe Asn Leu Leu Gln Gly Asn Leu Leu Lys
115 120 125

aat gcc cgc aag gtg gtg acc agc cgt ccg gcc gct gtg tcg gcg ttc 432
Asn Ala Arg Lys Val Val Thr Ser Arg Pro Ala Ala Val Ser Ala Phe
130 135 140

ctc agg aag tac atc cgc acc gag ttc aac ctc aag ggc ttc tct gaa 480
Leu Arg Lys Tyr Ile Arg Thr Glu Phe Asn Leu Lys Gly Phe Ser Glu
145 150 155 160

cag ggc atc gag ctg tac ctg agg aag cgc cat cat gag ccc ggg gtg 528
Gln Gly Ile Glu Leu Tyr Leu Arg Lys Arg His His Glu Pro Gly Val
165 170 175

gcg gac cgc ctc atc cgc ctg ctc caa gag acc tca gcc ctg cac ggt 576
Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser Ala Leu His Gly
180 185 190

ttg tgc cac ctg cct gtc ttc tca tgg atg gtg tcc aaa tgc cac cag 624
Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser Lys Cys His Gln
195 200 205

gaa ctg ttg ctg cag gag ggg ggg tcc cca aag acc act aca gat atg 672
Glu Leu Leu Leu Gln Glu Gly Ser Pro Lys Thr Thr Asp Met
210 215 220

tac ctg ctg att ctg cag cat ttt ctg ctg cat gcc acc ccc cca gac 720
Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala Thr Pro Pro Asp
225 230 235 240

tca gct tcc caa ggt ctg gga ccc agt ctt ctt cgg ggc cgc ctc ccc 768
Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg Gly Arg Leu Pro
245 250 255

acc ctc ctg cac ctg ggc aga ctg gct ctg tgg ggc ctg ggc atg tgc 816
Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly Leu Gly Met Cys
260 265 270

tgc tac gtg ttc tca gcc cag cag ctc cag gca gca cag gtc agc cct 864
Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala Gln Val Ser Pro
275 280 285

gat gac att tct ctt ggc ttc ctg 888
Asp Asp Ile Ser Leu Gly Phe Leu
290 295

<210> 174
<211> 296
<212> PRT
<213> Homo sapiens

<400> 174
Asp Asp Ala Asp Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly Lys
1 5 10 15
Ser Thr Leu Leu Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln Asp
20 25 30
Phe Gln Gln Phe Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu Gln
35 40 45
Cys Met Ala Lys Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His Cys
50 55 60
Cys Trp Pro Asp Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Leu Asp
65 70 75 80
His Pro Asp Arg Val Leu Leu Thr Phe Asp Gly Phe Asp Glu Phe Lys
85 90 95
Phe Arg Phe Thr Asp Arg Glu Arg His Cys Ser Pro Thr Asp Pro Thr
100 105 110
Ser Val Gln Thr Leu Leu Phe Asn Leu Leu Gln Gly Asn Leu Leu Lys
115 120 125
Asn Ala Arg Lys Val Val Thr Ser Arg Pro Ala Ala Val Ser Ala Phe
130 135 140
Leu Arg Lys Tyr Ile Arg Thr Glu Phe Asn Leu Lys Gly Phe Ser Glu
145 150 155 160
Gln Gly Ile Glu Leu Tyr Leu Arg Lys Arg His His Glu Pro Gly Val
165 170 175
Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser Ala Leu His Gly
180 185 190
Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser Lys Cys His Gln
195 200 205
Glu Leu Leu Leu Gln Glu Gly Gly Ser Pro Lys Thr Thr Thr Asp Met
210 215 220
Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala Thr Pro Pro Asp
225 230 235 240
Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg Gly Arg Leu Pro
245 250 255
Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly Leu Gly Met Cys
260 265 270
Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala Gln Val Ser Pro
275 280 285
Asp Asp Ile Ser Leu Gly Phe Leu
290 295

<210> 175
<211> 1209
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (1) . . . (1209)

<400> 175

gag ccc ggg gtg gcg gac cgc ctc atc cgc ctg ctc caa gag acc tca 48
Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser
1 5 10 15

gcc ctg cac ggt ttg tgc cac ctg cct gtc ttc tca tgg atg gtg tcc 96
Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser
20 25 30

aaa tgc cac cag gaa ctg ttg ctg cag gag ggg ggg tcc cca aag acc 144
Lys Cys His Gln Glu Leu Leu Gln Glu Gly Ser Pro Lys Thr
35 40 45

act aca gat atg tac ctg ctg att ctg cag cat ttt ctg ctg cat gcc 192
Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala
50 55 60

acc ccc cca gac tca gct tcc caa ggt ctg gga ccc agt ctt ctt cgg 240
Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg
65 70 75 80

ggc cgc ctc ccc acc ctc ctg cac ctg ggc aga ctg gct ctg tgg ggc 288
Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly
85 90 95

ctg ggc atg tgc tgc tac gtg ttc tca gcc cag cag ctc cag gca gca 336
Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala
100 105 110

cag gtc agc cct gat gac att tct ctt ggc ttc ctg gtg cgt gcc aaa 384
Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu Val Arg Ala Lys
115 120 125

gtt gtc gtg cca ggg agt acg gcg ccc ctg gaa ttc ctt cac atc act 432
Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe Leu His Ile Thr
130 135 140

ttc cag tgc ttc ttt gcc gcg ttc tac ctg gca ctc agt gct gat gtg 480
Phe Gln Cys Phe Ala Ala Phe Tyr Leu Ala Leu Ser Ala Asp Val
145 150 155 160

cca cca gct ttg ctc aga cac ctc ttc aat tgt ggc agg cca ggc aac 528
Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly Arg Pro Gly Asn
165 170 175

tca cca atg gcc agg ctc ctg ccc acg atg tgc atc cag gcc tcg gag 576
Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile Gln Ala Ser Glu
180 185 190

gga aag gac agc agc gtg gca gct ttg ctg cag aag gcc gag ccg cac 624
Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys Ala Glu Pro His

D C D F S E S E D E D D

	195	200	205	
aac ctt cag atc aca gca gcc ttc ctg gca ggg ctg ttg tcc cgg gag Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu Leu Ser Arg Glu	210	215	220	672
cac tgg ggc ctg ctg gct gag tgc cag aca tct gag aag gcc ctg ctc His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu Lys Ala Leu Leu	225	230	235	720
cgg cgc cag gcc tgt gcc cgc tgg tgt ctg gcc cgc agc ctc cgc aag Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg Ser Leu Arg Lys	245	250	255	768
cac ttc cac tcc atc ccg cca gct gca ccg ggt gag gcc aag agc gtg His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu Ala Lys Ser Val	260	265	270	816
cat gcc atg ccc ggg ttc atc tgg ctc atc cgg agc ctg tac gag atg His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met	275	280	285	864
cag gag gag cgg ctg gct cgg aag gct gca cgt ggc ctg aat gtt ggg Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly Leu Asn Val Gly	290	295	300	912
cac ctc aag ttg aca ttt tgc agt gtg ggc ccc act gag tgt gct gcc His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr Glu Cys Ala Ala	305	310	315	960
ctg gcc ttt gtg ctg cag cac ctc cgg ccc gtg gcc ctg cag ctg Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val Ala Leu Gln Leu	325	330	335	1008
gac tac aac tct gtg ggt gac att ggc gtg gag cag ctg ctg cct tgc Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln Leu Leu Pro Cys	340	345	350	1056
ctt ggt gtc tgc aag gct ctg tat ttg cgc gat aac aat atc tca gac Leu Gly Val Cys Lys Ala Leu Tyr Leu Arg Asp Asn Asn Ile Ser Asp	355	360	365	1104
cga ggc atc tgc aag ctc att gaa tgt gct ctt cac tgc gag caa ttg Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His Cys Glu Gln Leu	370	375	380	1152
cag aag tta gcg ctg ggg aat aac tac atc act gcc gcg gga gcc caa Gln Lys Leu Ala Leu Gly Asn Asn Tyr Ile Thr Ala Ala Gly Ala Gln	385	390	395	1200
gtg ctg gcc Val Leu Ala				1209

<210> 176
<211> 403
<212> PRT
<213> Homo sapiens

<400> 176
Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser
1 5 10 15
Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser
20 25 30
Lys Cys His Gln Glu Leu Leu Gln Glu Gly Ser Pro Lys Thr
35 40 45
Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala
50 55 60
Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg
65 70 75 80
Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly
85 90 95
Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala
100 105 110
Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu Val Arg Ala Lys
115 120 125
Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe Leu His Ile Thr
130 135 140
Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu Ser Ala Asp Val
145 150 155 160
Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly Arg Pro Gly Asn
165 170 175
Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile Gln Ala Ser Glu
180 185 190
Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys Ala Glu Pro His
195 200 205
Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu Leu Ser Arg Glu
210 215 220
His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu Lys Ala Leu Leu
225 230 235 240
Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg Ser Leu Arg Lys
245 250 255
His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu Ala Lys Ser Val
260 265 270
His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met
275 280 285
Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly Leu Asn Val Gly
290 295 300
His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr Glu Cys Ala Ala
305 310 315 320
Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val Ala Leu Gln Leu
325 330 335
Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln Leu Leu Pro Cys
340 345 350
Leu Gly Val Cys Lys Ala Leu Tyr Leu Arg Asp Asn Asn Ile Ser Asp

DRAFT - DRAFT

355 360 365
Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His Cys Glu Gln Leu
370 375 380
Gln Lys Leu Ala Leu Gly Asn Asn Tyr Ile Thr Ala Ala Gly Ala Gln
385 390 395 400
Val Leu Ala

<210> 177
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (261)

<400> 177
atg aat ttc ata aag gac aat agc cga gcc ctt att caa aga atg gga 48
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
1 5 10 15

atg act gtt ata aag caa atc aca gat gac cta ttt gta tgg aat gtt 96
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val
20 25 30

ctg aat cgc gaa gaa gta aac atc att tgc tgc gag aag gtg gag cag 144
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45

gat gct gct aga ggg atc att cac atg att ttg aaa aag ggt tca gag 192
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60

tcc tgt aac ctc ttt ctt aaa tcc ctt aag gag tgg aac tat cct cta 240
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80

ttt cag gac ttg aat gga caa 261
Phe Gln Asp Leu Asn Gly Gln
85

<210> 178
<211> 87
<212> PRT
<213> Homo sapiens

<400> 178
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
1 5 10 15
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val

20 25 30
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80
Phe Gln Asp Leu Asn Gly Gln
85

<210> 179
<211> 891
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (891)

5 10 15 48
ctt cag agc ccc tgc atc att gaa ggg gaa tct ggc aaa ggc aag tcc
Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser
1 5 10 15

act ctg ctg cag cgc att gcc atg ctc tgg ggc tcc gga aag tgc aag 96
Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys
20 25 30

gct ctg acc aag ttc aaa ttc gtc ttc ttc cgt ctc agc agg gcc 144
Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala
35 40 45

cag ggt gga ctt ttt gaa acc ctc tgt gat caa ctc ctg gat ata cct 192
Gln Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro
50 55 60

ggc aca atc agg aag cag aca ttc atg gcc atg ctg ctg aag ctg cgg 240
Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg
65 70 75 80

cag agg gtt ctt ttc ctt ctt gat ggc tac aat gaa ttc aag ccc cag 288
Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln
85 90 95

aac tgc cca gaa atc gaa gcc ctg ata aag gaa aac cac cgc ttc aag 336
Asn Cys Pro Glu Ile Glu Ala Leu Lys Glu Asn His Arg Phe Lys
100 105 110

aac atg gtc atc gtc acc act acc act gag tgc ctg agg cac ata cgg 384
Asn Met Val Ile Val Thr Thr Thr Glu Cys Leu Arg His Ile Arg
115 120 125

DRAFT - DRAFT

cag ttt ggt gcc ctg act gct gag gtg ggg gat atg aca gaa gac agc 432
Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser
130 135 140

gcc cag gct ctc atc cga gaa gtg ctg atc aag gag ctt gct gaa ggc 480
Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly
145 150 155 160

ttg ttg ctc caa att cag aaa tcc agg tgc ttg agg aat ctc atg aag 528
Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys
165 170 175

acc cct ctc ttt gtg gtc atc act tgt gca atc cag atg ggt gaa agt 576
Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser
180 185 190

gag ttc cac tct cac aca caa aca acg ctg ttc cat acc ttc tat gat 624
Glu Phe His Ser His Thr Gln Thr Leu Phe His Thr Phe Tyr Asp
195 200 205

ctg ttg ata cag aaa aac aaa cac aaa cat aaa ggt gtg gct gca agt 672
Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser
210 215 220

gac ttc att cgg agc ctg gac cac cgt gga gac cta gct ctg gag ggt 720
Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly
225 230 235 240

gtg ttc tcc cac aag ttt gat ttc gaa ctg cag gat gtg tcc agc gtg 768
Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val
245 250 255

aat gag gat gtc ctg ctg aca act ggg ctc ctc tgt aaa tat aca gct 816
Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala
260 265 270

caa agg ttc aag cca aag tat aaa ttc ttt cac aag tca ttc cag gag 864
Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu
275 280 285

tac aca gca gga cga aga ctc agc agt 891
Tyr Thr Ala Gly Arg Arg Leu Ser Ser
290 295

<210> 180

<211> 297

<212> PRT

<213> Homo sapiens

<400> 180

Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser
1 5 10 15

Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys
20 25 30
Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala
35 40 45
Gln Gly Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro
50 55 60
Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg
65 70 75 80
Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln
85 90 95
Asn Cys Pro Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys
100 105 110
Asn Met Val Ile Val Thr Thr Thr Glu Cys Leu Arg His Ile Arg
115 120 125
Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser
130 135 140
Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly
145 150 155 160
Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys
165 170 175
Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser
180 185 190
Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp
195 200 205
Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser
210 215 220
Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly
225 230 235 240
Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val
245 250 255
Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala
260 265 270
Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu
275 280 285
Tyr Thr Ala Gly Arg Arg Leu Ser Ser
290 295

<210> 181
<211> 618
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (618)

<400> 181
gg ttt aac aag aac ctt aca aag ctc ata atg gat aac ata aag atg 48
Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met
1 5 10 15

aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg aag 96

Asn Glu Glu Asp Ala Ile Lys Leu-Ala Glu Gly Leu Lys Asn Leu Lys
20 25 30

aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag gga 144
Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly
35 40 45

atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt gaa 192
Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu
50 55 60

gaa att caa tta gtc tcc tgc ttg tct gca aat gca gtg aaa atc 240
Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile
65 70 75 80

cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat tta 288
Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu
85 90 95

tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa ctg 336
Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu
100 105 110

atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg ccc 384
Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro
115 120 125

tgg ggc tgt gac gtg caa ggc agc ctg agc ctg ctg ttg aaa cat ttg 432
Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu
130 135 140

gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga ctc 480
Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu
145 150 155 160

aca gat aca gag att aga att tta ggt gca ttt ttg aag aac cct 528
Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro
165 170 175

ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc agt 576
Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser
180 185 190

gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag 618
Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys
195 200 205

09854-125202

<210> 182
<211> 206
<212> PRT
<213> Homo sapiens

<400> 182

Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met
1 5 10 15
Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys
20 25 30
Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly
35 40 45
Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu
50 55 60
Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile
65 70 75 80
Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu
85 90 95
Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu
100 105 110
Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro
115 120 125
Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu
130 135 140
Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu
145 150 155 160
Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro
165 170 175
Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser
180 185 190
Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys
195 200 205

<210> 183

<211> 165

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (165)

<400> 183

acc tac att ccc agc agg gct gta tct ttg ttc aac tgg aag cag 48
Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln
1 5 10 15

gaa ttc agg act ctg gag gtc aca ctc cggtt acg aat ttg aat 96
Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn
20 25 30

aag caa gat atc aga tat ctg ggg aaa ata ttc acg tct gcc aca acg 144
Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser
35 40 45

ctc agg ctg caa ata aag aga 165

Leu Arg Leu Gln Ile Lys Arg
50 55

<210> 184
<211> 55
<212> PRT
<213> Homo sapiens

<400> 184
Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln
1 5 10 15
Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn
20 25 30
Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser
35 40 45
Leu Arg Leu Gln Ile Lys Arg
50 55

<210> 185
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 185
gaaatgtgct cgcaggagg 19

<210> 186
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 186
gatgagcttc tgacaggccc 20

<210> 187
<211> 3063
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (2385)

<221> CDS
<222> (2389) ... (2928)

DRAFT: 100% IDENTICAL

<400> 187
 tgt gaa atg tgc tcg cag gag gct ttt cag gca cag agg agc cag ctg 48
 Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu
 1 5 10 15

 gtc gag ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg 96
 Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu
 20 25 30

 gac tgg ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc 144
 Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly
 35 40 45

 ttc cac ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg 192
 Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu
 50 55 60

 gac acc gtc tgg aat aag ggt act tgg gcc tgc cag aag ctc atc gcg 240
 Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala
 65 70 75 80

 gct gcc caa gaa gcc cag gcc gac agc cag tcc ccc aag ctg cat ggc 288
 Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly
 85 90 95

 tgc tgg gac ccc cac tgc ctc cac cca gcc cga gac ctg cag agt cac 336
 Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His
 100 105 110

 cgg cca gcc att gtc agg agg ctc cac agc cat gtg gag aac atg ctg 384
 Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu
 115 120 125

 gac ctg gca tgg gag cgg ggt ttc gtc agc cag tat gaa tgc gat gaa 432
 Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu
 130 135 140

 atc agg ttg ccg atc ttc aca ccg tcc cag agg gca aga agg ctg ctt 480
 Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu
 145 150 155 160

 gat ctt gcc acg gtg aaa gcg aat gga ttg gct gcc ttc ctt cta caa 528
 Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln
 165 170 175

 cat gtt cag gaa tta cca gtc cca ttg gcc ctg cct ttg gaa gct gcc 576
 His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala
 180 185 190

 aca tgc aag aag tat atg gcc aag ctg agg acc acg gtg tct gct cag 624
 Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln
 195 200 205

DRAFT

tct	cgc	ttc	ctc	agt	acc	tat	gat	gga	gca	gag	acg	ctc	tgc	ctg	gag	672
Ser	Arg	Phe	Leu	Ser	Thr	Tyr	Asp	Gly	Ala	Glu	Thr	Leu	Cys	Leu	Glu	
210					215										220	
gac	ata	tac	aca	gag	aat	gtc	ctg	gag	gtc	tgg	gca	gat	gtg	ggc	atg	720
Asp	Ile	Tyr	Thr	Glu	Asn	Val	Leu	Glu	Val	Trp	Ala	Asp	Val	Gly	Met	
225					230										240	
gct	gga	ccc	ccg	cag	aag	agc	cca	gcc	acc	ctg	ggc	ctg	gag	gag	ctc	768
Ala	Gly	Pro	Pro	Gln	Lys	Ser	Pro	Ala	Thr	Leu	Gly	Leu	Glu	Glu	Leu	
									245		250				255	
ttc	agc	acc	cct	ggc	cac	ctc	aat	gac	gat	gcg	gac	act	gtg	ctg	gtg	816
Phe	Ser	Thr	Pro	Gly	His	Leu	Asn	Asp	Asp	Ala	Asp	Thr	Val	Leu	Val	
					260				265						270	
gtg	ggt	gag	gcg	ggc	agt	ggc	aag	agc	acg	ctc	ctg	cag	cgg	ctg	cac	864
Val	Gly	Glu	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Gln	Arg	Leu	His	
					275				280						285	
ttg	ctg	tgg	gct	gca	ggg	caa	gac	ttc	cag	gaa	ttt	ctc	ttt	gtc	ttc	912
Leu	Leu	Trp	Ala	Ala	Gly	Gln	Asp	Phe	Gln	Glu	Phe	Leu	Phe	Val	Phe	
					290				295						300	
cca	ttc	agc	tgc	cg	cag	ctg	cag	tgc	atg	gcc	aaa	cca	ctc	tct	gtg	960
Pro	Phe	Ser	Cys	Arg	Gln	Leu	Gln	Cys	Met	Ala	Lys	Pro	Leu	Ser	Val	
					305				310						315	
cgg	act	cta	ctc	ttt	gag	cac	tgc	tgt	tgg	cct	gat	gtt	ggt	caa	gaa	1008
Arg	Thr	Leu	Leu	Phe	Glu	His	Cys	Cys	Trp	Pro	Asp	Val	Gly	Gln	Glu	
					325				330						335	
gac	atc	ttc	cag	tta	ctc	ctt	gac	cac	cct	gac	cgt	gtc	ctg	tta	acc	1056
Asp	Ile	Phe	Gln	Leu	Leu	Leu	Asp	His	Pro	Asp	Arg	Val	Leu	Leu	Thr	
					340				345						350	
ttt	gat	ggc	ttt	gac	gag	ttc	aag	ttc	agg	ttc	acg	gat	cgt	gaa	cgc	1104
Phe	Asp	Gly	Phe	Asp	Glu	Phe	Lys	Phe	Arg	Phe	Thr	Asp	Arg	Glu	Arg	
					355				360						365	
cac	tgc	tcc	ccg	acc	gac	ccc	acc	tct	gtc	cag	acc	ctg	ctc	ttc	aac	1152
His	Cys	Ser	Pro	Thr	Asp	Pro	Thr	Ser	Val	Gln	Thr	Leu	Leu	Phe	Asn	
					370				375						380	
ctt	ctg	cag	ggc	'aac	ctg	ctg	aag	aat	gcc	cgc	aag	gtg	gtg	acc	agc	1200
Leu	Leu	Gln	Gly	Asn	Leu	Leu	Lys	Asn	Ala	Arg	Lys	Val	Val	Thr	Ser	
					385				390						395	
cgt	ccg	gcc	gct	gtg	tcg	gcf	ttc	ctc	agg	aag	tac	atc	cgc	acc	gag	1248
Arg	Pro	Ala	Ala	Val	Ser	Ala	Phe	Leu	Arg	Lys	Tyr	Ile	Arg	Thr	Glu	
					405				410						415	

ttc aac ctc aag ggc ttc tct gaa cag ggc atc gag ctg tac ctg agg 1296
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg
420 425 430

aag cgc cat cat gag ccc ggg gtg gcg gac cgc ctc atc cgc ctg ctc 1344
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu
435 440 445

caa gag acc tca gcc ctg cac ggt ttg tgc cac ctg cct gtc ttc tca 1392
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser
450 455 460

tgg atg gtg tcc aaa tgc cac cag gaa ctg ttg ctg cag gag ggg ggg 1440
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Gln Glu Gly Gly
465 470 475 480

tcc cca aag acc act aca gat atg tac ctg ctg att ctg cag cat ttt 1488
Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe
485 490 495

ctg ctg cat gcc acc ccc cca gac tca gct tcc caa ggt ctg gga ccc 1536
Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro
500 505 510

agt ctt ctt cgg ggc cgc ccc acc ctc ctg cac ctg ggc aga ctg 1584
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu
515 520 525

gct ctg tgg ggc ctg ggc atg tgc tac gtg ttc tca gcc cag cag 1632
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln
530 535 540

ctc cag gca gca cag gtc agc cct gat gac att tct ctt ggc ttc ctg 1680
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu
545 550 555 560

gtg cgt gcc aaa ggt gtc gtg cca ggg agt acg gcg ccc ctg gaa ttc 1728
Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe
565 570 575

ctt cac atc act ttc cag tgc ttc ttt gcc gcg ttc tac ctg gca ctc 1776
Leu His Ile Thr Phe Gln Cys Phe Ala Ala Phe Tyr Leu Ala Leu
580 585 590

agt gct gat gtg cca cca gct ttg ctc aga cac ctc ttc aat tgt ggc 1824
Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly
595 600 605

agg cca ggc aac tca cca atg gcc agg ctc ctg ccc acg atg tgc atc 1872
Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile
610 615 620

cag gcc tcg gag gga aag gac agc agc gtg gca gct ttg ctg cag aag 1920

DRAFT - 12/20/1998

Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys
625 630 635 640

gcc gag ccg cac aac ctt cag atc aca gca gcc ttc ctg gca ggg ctg
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu
645 650 655

ttg tcc cg^g gag cac tgg ggc ctg ctg gct gag tgc cag aca tct gag
Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu
660 665 670

aag gcc ctg ctc cg^g cgc cag gcc tgt gcc cgc tgg tgt ctg gcc cgc
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg
675 680 685

agc ctc cgc aag cac ttc cac tcc atc cc^g cca gct gca cc^g ggt gag
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu
690 695 700

gcc aag agc gtg cat gcc atg ccc ggg ttc atc tgg ctc atc cc^g agc
Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser
705 710 715 720

ctg tac gag atg cag gag gag cc^g ctg gct cc^g aag gct gca cgt ggc
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly
725 730 735

ctg aat gtt ggg cac ctc aag ttg aca ttt tgc agt gtg ggc ccc act
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr
740 745 750

gag tgt gct gcc ctg gcc ttt gtg ctg cag cac ctc cc^g cc^g ccc gtg
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val
755 760 765

gcc ctg cag ctg gac tac aac tct gtg ggt gac att ggc gtg gag cag
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln
770 775 780

ctg ctg cct tgc ctt ggt gtc tgc aag gct ctg taa ttc tgg ggc aac
Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu Phe Trp Gly Asn
785 790 795

aga gtg ggt gac gag ggg gcc cag gcc ctg gct gaa gcc ttg ggt gat
Arg Val Gly Asp Glu Gly Ala Gln Ala Leu Ala Glu Ala Leu Gly Asp
800 805 810 815

cac cag agc ttg agg tgg ctc agc ctg gtg ggg aac aac att ggc agt
His Gln Ser Leu Arg Trp Leu Ser Leu Val Gly Asn Asn Ile Gly Ser
820 825 830

gtg ggt gcc caa gcc ttg gca ctg atg ctg gca aag aac gtc atg cta
Val Gly Ala Gln Ala Leu Ala Leu Met Leu Ala Lys Asn Val Met Leu
840 845 850

835	840	845	
gaa gaa ctc tgc ctg gag gag aac cat ctc cag gat gaa ggt gta tgt Glu Glu Leu Cys Leu Glu Glu Asn His Leu Gln Asp Glu Gly Val Cys 850	855	860	2592
tct ctc gca gaa gga ctg aag aaa aat tca agt ttg aaa atc ctg aac Ser Leu Ala Glu Gly Leu Lys Lys Asn Ser Ser Leu Lys Ile Leu Asn 865	870	875	2640
ata aaa att cat gct tcg gga ttc aac aaa ctc ttg gaa agc att ttc Ile Lys Ile His Ala Ser Gly Phe Asn Lys Leu Leu Glu Ser Ile Phe 880	885	890	2688
tgc atc ctc ctg gtt gtg gaa gca ttt ttc ctg cag aaa gtt gtc aag Cys Ile Leu Leu Val Val Glu Ala Phe Phe Leu Gln Lys Val Val Lys 900	905	910	2736
att ctt gaa gaa atg gta gtc agt tgg cta gag gtc agg ttg tcc aat Ile Leu Glu Glu Met Val Val Ser Trp Leu Glu Val Arg Leu Ser Asn 915	920	925	2784
aac tgc atc acc tac cta ggg gca gaa gcc ctc ctg cag gcc ctt gaa Asn Cys Ile Thr Tyr Leu Gly Ala Glu Ala Leu Leu Gln Ala Leu Glu 930	935	940	2832
agg aat gac acc atc ctg gaa gtc tgg ctc cga ggg aac act ttc tct Arg Asn Asp Thr Ile Leu Glu Val Trp Leu Arg Gly Asn Thr Phe Ser 945	950	955	2880
cta gag gag gtt gac aag ctc ggc tgc agg gac acc aga ctc ttg ctt Leu Glu Glu Val Asp Lys Leu Gly Cys Arg Asp Thr Arg Leu Leu Leu 960	965	970	2928
tgaagtctcc gggaggatgt tcgtctcagt ttgttgtga gcaggctgtg agtttggcc 2988 ccagaggctg ggtgacatgt gttggcagcc tottcaaaat gagccctgtc ctgcctaagg 3048 ctgaacttgt ttct 3063			
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Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu 1 5 10 15			
Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu 20 25 30			
Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly 35 40 45			
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu 50 55 60			
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala			

TOP SECRET//NOFORN

65	70	75	80
Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly			
85	90	95	
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His			
100	105	110	
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu			
115	120	125	
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu			
130	135	140	
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu			
145	150	155	160
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln			
165	170	175	
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala			
180	185	190	
Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln			
195	200	205	
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu			
210	215	220	
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met			
225	230	235	240
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu			
245	250	255	
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val			
260	265	270	
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His			
275	280	285	
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe			
290	295	300	
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val			
305	310	315	320
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu			
325	330	335	
Asp Ile Phe Gln Leu Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr			
340	345	350	
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg			
355	360	365	
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn			
370	375	380	
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser			
385	390	395	400
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu			
405	410	415	
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg			
420	425	430	
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu			
435	440	445	
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser			
450	455	460	
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Gln Glu Gly Gly			
465	470	475	480
Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe			
485	490	495	

Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro
500 505 510
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu
515 520 525
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln
530 535 540
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu
545 550 555 560
Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe
565 570 575
Leu His Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu
580 585 590
Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly
595 600 605
Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile
610 615 620
Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys
625 630 635 640
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu
645 650 655
Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu
660 665 670
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg
675 680 685
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu
690 695 700
Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser
705 710 715 720
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly
725 730 735
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr
740 745 750
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val
755 760 765
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln
770 775 780
Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu
785 790 795

<210> 189
<211> 180
<212> PRT
<213> Homo sapiens

<400> 189
Phe Trp Gly Asn Arg Val Gly Asp Glu Gly Ala Gln Ala Leu Ala Glu
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Ala Leu Gly Asp His Gln Ser Leu Arg Trp Leu Ser Leu Val Gly Asn
20 25 30
Asn Ile Gly Ser Val Gly Ala Gln Ala Leu Ala Leu Met Leu Ala Lys
35 40 45
Asn Val Met Leu Glu Glu Leu Cys Leu Glu Glu Asn His Leu Gln Asp

50	55	60													
Glu	Gly	Val	Cys	Ser	Leu	Ala	Glu	Gly	Leu	Lys	Lys	Asn	Ser	Ser	Leu
65					70				75						80
Lys	Ile	Leu	Asn	Ile	Lys	Ile	His	Ala	Ser	Gly	Phe	Asn	Lys	Leu	Leu
					85				90					95	
Glu	Ser	Ile	Phe	Cys	Ile	Leu	Leu	Val	Val	Glu	Ala	Phe	Phe	Leu	Gln
					100			105						110	
Lys	Val	Val	Lys	Ile	Leu	Glu	Glu	Met	Val	Val	Ser	Trp	Leu	Glu	Val
					115			120					125		
Arg	Leu	Ser	Asn	Asn	Cys	Ile	Thr	Tyr	Leu	Gly	Ala	Glu	Ala	Leu	Leu
					130			135				140			
Gln	Ala	Leu	Glu	Arg	Asn	Asp	Thr	Ile	Leu	Glu	Val	Trp	Leu	Arg	Gly
					145			150				155		160	
Asn	Thr	Phe	Ser	Leu	Glu	Glu	Val	Asp	Lys	Leu	Gly	Cys	Arg	Asp	Thr
					165				170					175	
Arg	Leu	Leu	Leu												
					180										

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<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (193) ... (612)

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gctgacacat cggtggcctc tctcaagcac ctttcagct gtggccggct gggcagctca 120
ctgctggaa ggctgctgcc caaccctgtgt atccagggct ccagagtcaa gaagggcagc 180

gaagcagccc tg ctg cag aag gct gag cca cac aac ctg caa atc aca gca 231
Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala

1 5 10

gcc ttc cta gca ggt ctg ttg tcc cag cag cat cgg gac ctg ttg gct 279
Ala Phe Leu Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Ala
15 20 25

gca tgc cag gtc tcc gag agg gta ctg ctc cag cgt cag gca cgt gcc 327
Ala Cys Gln Val Ser Glu Arg Val Leu Gln Arg Gln Ala Arg Ala
30 35 40 45

cgc tcg tgt ctg gcc cac agc ctc cgc gag cac ttc cat tcc atc ccg 375
Arg Ser Cys Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro
50 55 60

cct gcc gtg ccc ggt gag acc aag agc atg cat gct atg ccg ggc ttc 423
Pro Ala Val Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe
65 70 75

att tgg ctc atc cgt agc ctg tac gag atg cag gag gag cag ttg gcc 471

Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala
80 85 90

cag gag gct gtc cgt cgc ttg gac atc ggg cac ctg aag ttg aca ttt 519
Gln Glu Ala Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe
95 100 105

tgc aga gtg ggc cct gca gag tgt gct gca ctg gcc ttt gta ctg caa 567
Cys Arg Val Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln
110 115 120 125

cat ctc cag cgg cct gtg gcc cta cag ctg gat tac aac tct gtg 612
His Leu Gln Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser Val
130 135 140

ggagatgttg ggagtggaac agctgcgacc gtgccttgg ggtctgcaca gctctgtagt 672
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<211> 140

<212> PRT

<213> Mus musculus

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Val Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala Arg Ser Cys
35 40 45
Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro Pro Ala Val
50 55 60
Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe Ile Trp Leu
65 70 75 80
Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala Gln Glu Ala
85 90 95
Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe Cys Arg Val
100 105 110
Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Gln
115 120 125
Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser Val
130 135 140

<210> 192

<211> 419

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(417)

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Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu
1 5 10 15

gca ggt ctg ttg tcc cag cag cat cgg gac ctg ttg gct gca tgc cag 96
Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Leu Ala Ala Cys Gln
20 25 30

atc tcc gag agg gtg ctg ctc cag cgt cag gca cgt gcc cgcc tcg tgt 144
Ile Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala Arg Ser Cys
35 40 45

ctg gcc cac agc ctc cgc gag cac ttc cat tcc atc ccg cct gcc gtg 192
Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro Pro Ala Val
50 55 60

ccc ggt gag acc aag agc atg cat gct atg ccg ggc ttt att tgg ctc 240
Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe Ile Trp Leu
65 70 75 80

atc cgg agc ctg tac gag atg cag gag cag ttg gcc cag gag gct 288
Ile Arg Ser Leu Tyr Glu Met Gln Glu Gln Leu Ala Gln Glu Ala
85 90 95

gtc cgt cgc ttg gac atc ggg cac ctg aag ttg aca ttt tgc aga gtg 336
Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe Cys Arg Val
100 105 110

ggc cct gca gag tgt gct gcg ctg gcc ttt gta ctg caa cat ctc cag 384
Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Gln
115 120 125

cgg cct gtg gcc cta cag ctg gat tac aac tct gt 419
Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser
130 135

<210> 193

<211> 139

<212> PRT

<213> Mus musculus

<400> 193

Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu
1 5 10 15
Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Leu Ala Ala Cys Gln
20 25 30
Ile Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala Arg Ser Cys
35 40 45
Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro Pro Ala Val
50 55 60
Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe Ile Trp Leu

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65	70	75	80
Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala Gln Glu Ala			
	85	90	95
Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe Cys Arg Val			
	100	105	110
Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Gln			
	115	120	125
Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser			
	130	135	

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26

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<210> 195  
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<220>
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<400> 195
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30